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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=3; day=30; hr=11; min=3; sec=6; ms=676;]

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Application No: 10561108 Version No: 2.0

Input Set:

Output Set:

Started: 2010-03-22 18:28:05.814
Finished: 2010-03-22 18:28:12.571
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 757 ms
Total Warnings: 22
Total Errors: 18
No. of SeqIDs Defined: 22
Actual SeqID Count: 22

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
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E 257	Invalid sequence data feature in <221> in SEQ ID (1)
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E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)

Input Set:

Output Set:

Started: 2010-03-22 18:28:05.814
Finished: 2010-03-22 18:28:12.571
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 757 ms
Total Warnings: 22
Total Errors: 18
No. of SeqIDs Defined: 22
Actual SeqID Count: 22

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> BURKART, MICHAEL D.
LACLAIR, JAMES J.

<120> COMPOSITIONS AND METHODS FOR ANALYSIS AND MANIPULATION OF
ENZYMES IN BIOSYNTHETIC PROTEOMES

<130> 26774-14255/US

<140> 10561108

<141> 2006-05-11

<150> PCT/US2004/019568

<151> 2004-06-17

<150> 60/479,344

<151> 2003-06-17

<160> 22

<170> PatentIn version 3.5

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<211> 16

<212> PRT

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<220>

<223> Description of Artificial Sequence: Synthetic
consensus sequence

<220>

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<222> (2)..(2)

<223> Leu, Ile, Val, Met, Phe, Tyr, Ser, Thr, Ala or Cys

<220>

<221> MOD_RES

<222> (3)..(3)

<223> Gly, Asn or Gln

<220>

<221> MOD_RES

<222> (4)..(4)

<223> Leu, Ile, Val, Met, Phe, Tyr, Ala or Gly

<220>

<221> MOD_RES

<222> (5)..(5)

<223> Asp, Asn, Glu, Lys, His or Ser

<220>

<221> MOD_RES

<222> (7)..(7)

<223> Leu, Ile, Val, Met, Ser or Thr

<220>

<221> MOD_RES

<222> (8)..(8)

<223> Any amino acid except Pro, Cys, Phe or Tyr

<220>

<221> MOD_RES

<222> (9)..(9)

<223> Ser, Thr, Ala, Gly, Cys, Pro, Gln, Leu, Ile, Val, Met or Phe

<220>

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<222> (10)..(10)

<223> Leu, Ile, Val, Met, Ala, Thr or Asn

<220>

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<222> (11)..(11)

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<220>

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<222> (13)..(13)

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<220>

<221> MOD_RES

<222> (14)..(15)

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<222> (16)..(16)

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1

5

10

15

<210> 2

<211> 10

<212> PRT

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<220>
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peptide

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1 5 10

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<212> PRT
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<220>
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peptide

<220>
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<222> (2)..(2)
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<222> (6)..(6)
<223> Gly or absent

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Phe Xaa Pro Arg Leu Xaa
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<210> 4
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peptide

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<222> (2)..(2)
<223> Gly, Ser, Thr or Val

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<210> 5
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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<220>

<221> MOD_RES

<222> (2)..(2)

<223> Gly, Ser, Thr or Val

<400> 5

Phe Xaa Pro Arg Leu

1 5

<210> 6

<211> 16

<212> PRT

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<220>

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peptide

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1 5 10 15

<210> 7

<211> 16

<212> PRT

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peptide

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<211> 16

<212> PRT

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<223> Description of Artificial Sequence: Synthetic
peptide

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<220>
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peptide

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1 5 10 15

<210> 10
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peptide

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1 5 10 15

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peptide

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<210> 12
<211> 16
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

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1 5 10 15

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<220>
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peptide

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1 5 10 15

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<220>
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peptide

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1 5 10 15

<210> 15
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

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Glu Leu Gly Gly Asp Ser Ile Lys Ala Ile Gln Val Ser Thr Arg Leu
1 5 10 15

<210> 16
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

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Asp Leu Gly Gly His Ser Leu Lys Ala Met Thr Val Val Phe Gln Val
1 5 10 15

<210> 17
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

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<210> 18
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 18
Gln Ile Gly Gly His Ser Leu Lys Ala Met Ala Val Ala Ala Gln Val
1 5 10 15

<210> 19
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 19
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1 5 10 15

<210> 20
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

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1 5 10 15

<210> 21

<211> 16
<212> PRT
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<220>
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1 5 10 15

<210> 22
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide

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1 5 10 15

Thr Cys Glu Lys Asn Ile Val Ala Cys Glu Arg Asp Leu Ala Ala Ser
20 25 30

Cys Pro Asp Arg Asp Leu Phe Arg Ala Phe Thr Ser Gly Met Ile Ile
35 40 45

Arg Lys Leu Arg Gln Arg Asp Gly Ile Asp Ile Asp Thr Pro Leu Gln
50 55 60

Ala Leu Gln Lys Leu Ala Ala Gln Gly Tyr Gln Asp Val Ala Ile Gln
65 70 75 80